of commercial gateways or other similar uses is prohibited and may result in loss of user privileges and other penalties.

* * * * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 12:49:11 ON 10 FEB 2007

=> file medline, biosis
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 12:49:32 ON 10 FEB 2007

FILE 'BIOSIS' ENTERED AT 12:49:32 ON 10 FEB 2007
Copyright (c) 2007 The Thomson Corporation

=> s (intracellular recognition molecule) and (peptide aptamer)
L1 0 (INTRACELLULAR RECOGNITION MOLECULE) AND (PEPTIDE APTAMER)

=> s (TRX and TRX-like protein)
L2 2 (TRX AND TRX-LIKE PROTEIN)

=> d l2 ti abs ibib tot

L2 ANSWER 1 OF 2 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
TI Dim2, a new TRX-like protein implicated in cell cycle progression.
ACCESSION NUMBER: 2005:301677 BIOSIS
DOCUMENT NUMBER: PREV200510095702
TITLE: Dim2, a new TRX-like protein implicated in cell cycle progression.
AUTHOR(S): Simeoni, F. [Reprint Author]; Bello, P.; Gondeau, C.; Neyroz, P.; Tainer, J.; Heitz, F.; Divita, G.
CORPORATE SOURCE: CNRS, CRBM, F-34033 Montpellier, France
SOURCE: Molecular Biology of the Cell, (NOV 2004) Vol. 15, No. Suppl. S, pp. 369A.
Meeting Info.: 44th Annual Meeting of the American-Society-for-Cell-Biology. Washington, DC, USA. December 04 -08, 2004. Amer Soc Cell Biol.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 15 Aug 2005
Last Updated on STN: 15 Aug 2005

L2 ANSWER 2 OF 2 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
TI Structural and functional analysis of a new Trx-like protein, Dim2.
ACCESSION NUMBER: 2002:365253 BIOSIS
DOCUMENT NUMBER: PREV200200365253
TITLE: Structural and functional analysis of a new Trx-like protein, Dim2.
AUTHOR(S): Simeoni, Federica [Reprint author]; Bello, Paul [Reprint author]; Gondeau, Claire [Reprint author]; Hopfner, Karl-Peter; Neyroz, Paolo; Tainer, John; Divita, Gilles [Reprint author]
CORPORATE SOURCE: CNRS, 1919, Route de Mende, Montpellier, 34293, France
SOURCE: Biophysical Journal, (January, 2002) Vol. 82, No. 1 Part 2, pp. 453a. print.
Meeting Info.: 46th Annual Meeting of the Biophysical Society. San Francisco, California, USA. February 23-27, 2002.

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspta1653hxp

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2		"Ask CAS" for self-help around the clock
NEWS 3	OCT 23	The Derwent World Patents Index suite of databases on STN has been enhanced and reloaded
NEWS 4	OCT 30	CHEMLIST enhanced with new search and display field
NEWS 5	NOV 03	JAPIO enhanced with IPC 8 features and functionality
NEWS 6	NOV 10	CA/CAplus F-Term thesaurus enhanced
NEWS 7	NOV 10	STN Express with Discover! free maintenance release Version 8.01c now available
NEWS 8	NOV 20	CA/CAplus to MARPAT accession number crossover limit increased to 50,000
NEWS 9	DEC 01	CAS REGISTRY updated with new ambiguity codes
NEWS 10	DEC 11	CAS REGISTRY chemical nomenclature enhanced
NEWS 11	DEC 14	WPIDS/WPINDEX/WPIX manual codes updated
NEWS 12	DEC 14	GBFULL and FRFULL enhanced with IPC 8 features and functionality
NEWS 13	DEC 18	CA/CAplus pre-1967 chemical substance index entries enhanced with preparation role
NEWS 14	DEC 18	CA/CAplus patent kind codes updated
NEWS 15	DEC 18	MARPAT to CA/CAplus accession number crossover limit increased to 50,000
NEWS 16	DEC 18	MEDLINE updated in preparation for 2007 reload
NEWS 17	DEC 27	CA/CAplus enhanced with more pre-1907 records
NEWS 18	JAN 08	CHEMLIST enhanced with New Zealand Inventory of Chemicals
NEWS 19	JAN 16	CA/CAplus Company Name Thesaurus enhanced and reloaded
NEWS 20	JAN 16	IPC version 2007.01 thesaurus available on STN
NEWS 21	JAN 16	WPIDS/WPINDEX/WPIX enhanced with IPC 8 reclassification data
NEWS 22	JAN 22	CA/CAplus updated with revised CAS roles
NEWS 23	JAN 22	CA/CAplus enhanced with patent applications from India
NEWS 24	JAN 29	PHAR reloaded with new search and display fields
NEWS 25	JAN 29	CAS Registry Number crossover limit increased to 300,000 in multiple databases

NEWS EXPRESS	NOVEMBER 10 CURRENT WINDOWS VERSION IS V8.01c, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 25 SEPTEMBER 2006.
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS LOGIN	Welcome Banner and News Items
NEWS IPC8	For general information regarding STN implementation of IPC 8
NEWS X25	X.25 communication option no longer available

Enter NEWS followed by the item number or name to see news on that specific topic.

All use of STN is subject to the provisions of the STN Customer agreement. Please note that this agreement limits use to scientific research. Use for software development or design or implementation

```
                    CODEN: BIOJAU. ISSN: 0006-3495.
DOCUMENT TYPE:      Conference; (Meeting)
                    Conference; Abstract; (Meeting Abstract)
                    Conference; (Meeting Poster)
LANGUAGE:           English
ENTRY DATE:         Entered STN: 3 Jul 2002
                    Last Updated on STN: 3 Jul 2002


=> d his

     (FILE 'HOME' ENTERED AT 12:49:11 ON 10 FEB 2007)

     FILE 'MEDLINE, BIOSIS' ENTERED AT 12:49:32 ON 10 FEB 2007
L1             0 S (INTRACELLULAR RECOGNITION MOLECULE) AND (PEPTIDE APTAMER)
L2             2 S (TRX AND TRX-LIKE PROTEIN)

=> s (thioredoxin and TRX-like protein)
L3             1 (THIOREDOXIN AND TRX-LIKE PROTEIN)

=> d l3 ti abs ibib tot

L3   ANSWER 1 OF 1  BIOSIS  COPYRIGHT (c) 2007 The Thomson Corporation  on STN
TI   Dim2, a new TRX-like protein implicated in
     cell cycle progression.
ACCESSION NUMBER:   2005:301677  BIOSIS
DOCUMENT NUMBER:    PREV200510095702
TITLE:              Dim2, a new TRX-like protein
                    implicated in cell cycle progression.
AUTHOR(S):          Simeoni, F. [Reprint Author]; Bello, P.; Gondeau, C.;
                    Neyroz, P.; Tainer, J.; Heitz, F.; Divita, G.
CORPORATE SOURCE:   CNRS, CRBM, F-34033 Montpellier, France
SOURCE:             Molecular Biology of the Cell, (NOV 2004) Vol. 15, No.
                    Suppl. S, pp. 369A.
                    Meeting Info.: 44th Annual Meeting of the
                    American-Society-for-Cell-Biology. Washington, DC, USA.
                    December 04 -08, 2004. Amer Soc Cell Biol.
                    CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE:      Conference; (Meeting)
                    Conference; Abstract; (Meeting Abstract)
LANGUAGE:           English
ENTRY DATE:         Entered STN: 15 Aug 2005
                    Last Updated on STN: 15 Aug 2005


=> d his

     (FILE 'HOME' ENTERED AT 12:49:11 ON 10 FEB 2007)

     FILE 'MEDLINE, BIOSIS' ENTERED AT 12:49:32 ON 10 FEB 2007
L1             0 S (INTRACELLULAR RECOGNITION MOLECULE) AND (PEPTIDE APTAMER)
L2             2 S (TRX AND TRX-LIKE PROTEIN)
L3             1 S (THIOREDOXIN AND TRX-LIKE PROTEIN)

=> s thioredoxin
L4          9702 THIOREDOXIN

=> d l4 and l1
L1 IS NOT VALID HERE
For an explanation, enter "HELP DISPLAY".

=> d his

     (FILE 'HOME' ENTERED AT 12:49:11 ON 10 FEB 2007)
```

```
     FILE 'MEDLINE, BIOSIS' ENTERED AT 12:49:32 ON 10 FEB 2007
L1             0 S (INTRACELLULAR RECOGNITION MOLECULE) AND (PEPTIDE APTAMER)
L2             2 S (TRX AND TRX-LIKE PROTEIN)
L3             1 S (THIOREDOXIN AND TRX-LIKE PROTEIN)
L4          9702 S THIOREDOXIN

=> s l4 and (cdk2)
L5             7 L4 AND (CDK2)

=> d l5 ti abs ibib tot

L5   ANSWER 1 OF 7     MEDLINE on STN
TI   Production of soluble mammalian proteins in Escherichia coli:
     identification of protein features that correlate with successful
     expression.
AB   BACKGROUND: In the search for generic expression strategies for mammalian
     protein families several bacterial expression vectors were examined for
     their ability to promote high yields of soluble protein. Proteins studied
     included cell surface receptors (Ephrins and Eph receptors, CD44), kinases
     (EGFR-cytoplasmic domain, CDK2 and 4), proteases (MMP1, CASP2),
     signal transduction proteins (GRB2, RAF1, HRAS) and transcription factors
     (GATA2, Fli1, Trp53, Mdm2, JUN, FOS, MAD, MAX). Over 400 experiments were
     performed where expression of 30 full-length proteins and protein domains
     were evaluated with 6 different N-terminal and 8 C-terminal fusion
     partners. Expression of an additional set of 95 mammalian proteins was
     also performed to test the conclusions of this study. RESULTS: Several
     protein features correlated with soluble protein expression yield
     including molecular weight and the number of contiguous hydrophobic
     residues and low complexity regions. There was no relationship between
     successful expression and protein pI, grand average of hydropathicity
     (GRAVY), or sub-cellular location. Only small globular cytoplasmic
     proteins with an average molecular weight of 23 kDa did not require a
     solubility enhancing tag for high level soluble expression.
     Thioredoxin (Trx) and maltose binding protein (MBP) were the best
     N-terminal protein fusions to promote soluble expression, but MBP was most
     effective as a C-terminal fusion. 63 of 95 mammalian proteins expressed at
     soluble levels of greater than 1 mg/l as N-terminal H10-MBP fusions and
     those that failed possessed, on average, a higher molecular weight and
     greater number of contiguous hydrophobic amino acids and low complexity
     regions. CONCLUSIONS: By analysis of the protein features identified
     here, this study will help predict which mammalian proteins and domains
     can be successfully expressed in E. coli as soluble product and also which
     are best targeted for a eukaryotic expression system. In some cases
     proteins may be truncated to minimise molecular weight and the numbers of
     contiguous hydrophobic amino acids and low complexity regions to aid
     soluble expression in E. coli.
ACCESSION NUMBER:    2005032544     MEDLINE
DOCUMENT NUMBER:     PubMed ID: 15598350
TITLE:               Production of soluble mammalian proteins in Escherichia
                     coli: identification of protein features that correlate
                     with successful expression.
AUTHOR:              Dyson Michael R; Shadbolt S Paul; Vincent Karen J; Perera
                     Rajika L; McCafferty John
CORPORATE SOURCE:    The Atlas of Gene Expression Project, The Wellcome Trust
                     Sanger Institute, Wellcome Trust Genome Campus, Hinxton,
                     Cambridge, CB10 1SA, UK.. mrd@sanger.ac.uk
SOURCE:              BMC biotechnology [electronic resource], (2004 Dec 14) Vol.
                     4, pp. 32.  Electronic Publication: 2004-12-14.
                     Journal code: 101088663. E-ISSN: 1472-6750.
PUB. COUNTRY:        England: United Kingdom
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
```

ENTRY MONTH: 200601
ENTRY DATE: Entered STN: 25 Jan 2005
Last Updated on STN: 14 Dec 2005
Entered Medline: 26 Jan 2006

L5 ANSWER 2 OF 7 MEDLINE on STN
TI Engineered protein scaffolds for molecular recognition.
AB The use of so-called protein scaffolds has recently attracted considerable attention in biochemistry in the context of generating novel types of ligand receptors for various applications in research and medicine. This development started with the notion that immunoglobulins owe their function to the composition of a conserved framework region and a spatially well-defined antigen-binding site made of peptide segments that are hypervariable both in sequence and in conformation. After the application of antibody engineering methods along with library techniques had resulted in first successes in the selection of functional antibody fragments, several laboratories began to exploit other types of protein architectures for the construction of practically useful binding proteins. Properties like small size of the receptor protein, stability and ease of production were the focus of this work. Hence, among others, single domains of antibodies or of the immunoglobulin superfamily, protease inhibitors, helix-bundle proteins, disulphide-knotted peptides and lipocalins were investigated. Recently, the scaffold concept has even been adopted for the construction of enzymes. However, it appears that not all kinds of polypeptide fold which may appear attractive for the engineering of loop regions at a first glance will indeed permit the construction of independent ligand-binding sites with high affinities and specificities. This review will therefore concentrate on the critical description of the structural properties of experimentally tested protein scaffolds and of the novel functions that have been achieved on their basis, rather than on the methodology of how to best select a particular mutant with a certain activity. An overview will be provided about the current approaches, and some emerging trends will be identified. (c) 2000 John Wiley & Sons, Ltd. Abbreviations used: ABD albumin-binding domain of protein G APPI Alzheimer's amyloid beta-protein precursor inhibitor BBP bilin-binding protein BPTI bovine (or basic) pancreatic trypsin inhibitor BSA bovine serum albumin CBD cellulose-binding domain of cellobiohydrolase I CD circular dichroism Cdk2 human cyclin-dependent kinase 2 CDR complementarity-determining region CTLA-4 human cytotoxic T-lymphocyte associated protein-4 FN3 fibronectin type III domain GSH glutathione GST glutathione S-transferase hIL-6 human interleukin-6 HSA human serum albumin IC(50) half-maximal inhibitory concentration Ig immunoglobulin IMAC immobilized metal affinity chromatography K(D) equilibrium constant of dissociation K(i) equilibrium dissociation constant of enzyme inhibitor LACI-D1 human lipoprotein-associated coagulation inhibitor pIII gene III minor coat protein from filamentous bacteriophage f1 PCR polymerase-chain reaction PDB Protein Data Bank PSTI human pancreatic secretory trypsin inhibitor RBP retinol-binding protein SPR surface plasmon resonance TrxA E. coli thioredoxin
ACCESSION NUMBER: 2000424395 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10931555
TITLE: Engineered protein scaffolds for molecular recognition.
AUTHOR: Skerra A
CORPORATE SOURCE: Lehrstuhl fur Biologische Chemie, Technische Universitat Munchen, D-85350 Freising-Weihenstephan, Germany.. Skerra@Weihenstephan.de
SOURCE: Journal of molecular recognition : JMR, (2000 Jul-Aug) Vol. 13, No. 4, pp. 167-87. Ref: 115
Journal code: 9004580. ISSN: 0952-3499.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 22 Sep 2000
Last Updated on STN: 23 Jul 2001
Entered Medline: 14 Sep 2000

L5 ANSWER 3 OF 7 MEDLINE on STN

TI Selenium metabolism, selenoproteins and mechanisms of cancer prevention: complexities with thioredoxin reductase.

AB Numerous studies in animal models and more recent studies in humans have demonstrated cancer chemopreventive effects with Se. There is extensive evidence that monomethylated forms of Se are critical metabolites for chemopreventive effects of Se. Induction of apoptosis in transformed cells is an important chemopreventive mechanism. Apoptosis can be triggered by micromolar levels of monomethylated forms of Se independent of DNA damage and in cells having a null p53 phenotype. Cell cycle protein kinase cdk2 and protein kinase C are strongly inhibited by various forms of Se. Inhibitory mechanisms involving modification of cysteine residues in proteins by Se have been proposed that involve formation of Se adducts of the selenotrisulfide (S-Se-S) or selenenylsulfide (S-Se) type or catalysis of disulfide formation. Selenium may facilitate reactions of protein cysteine residues by the transient formation of more reactive S-Se intermediates. A novel chemopreventive mechanism is proposed involving Se catalysis of reversible cysteine/disulfide transformations that occur in a number of redox-regulated proteins, including transcription factors. A time-limited activation mechanism for such proteins, with deactivation facilitated by Se, would allow normalization of critical cellular processes in the early stages of transformation. There is uncertainty at the present time regarding the role of selenoproteins in chemoprevention model systems where supranutritional levels of Se are employed. Mammalian thioredoxin reductase is one selenoprotein that shows increased activity with Se supplementation in the nutritional to supranutritional range. Enhanced thioredoxin reduction could have beneficial effects in oxidative stress, but possible adverse effects are considered. Other functions of thioredoxin reductase may be relevant to cell signaling pathways. The functional status of the thioredoxin/thioredoxin reductase system during in vivo chemoprevention with Se has not been established. Some in vitro studies have shown inhibitory effects of Se on the thioredoxin system correlated with growth inhibition by Se. A potential inactivating mechanism for thioredoxin reductase or other selenoenzymes involving formation of a stable diselenide form resistant to reduction is discussed. New aspects of Se biochemistry and possible functions of new selenoproteins in chemoprevention are described.

ACCESSION NUMBER: 1999400568 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10469608
TITLE: Selenium metabolism, selenoproteins and mechanisms of cancer prevention: complexities with thioredoxin reductase.
AUTHOR: Ganther H E
CORPORATE SOURCE: Department of Nutritional Sciences, University of Wisconsin, 1415 Linden Drive, Madison, WI 53706, USA.. hganther@facstaff.wisc.edu
CONTRACT NUMBER: CA 45164 (NCI)
SOURCE: Carcinogenesis, (1999 Sep) Vol. 20, No. 9, pp. 1657-66.
Ref: 86
Journal code: 8008055. ISSN: 0143-3334.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199909
ENTRY DATE: Entered STN: 12 Oct 1999

Last Updated on STN: 3 Mar 2000
Entered Medline: 30 Sep 1999

L5 ANSWER 4 OF 7 MEDLINE on STN
TI Genetic selection of peptide aptamers that recognize and inhibit cyclin-dependent kinase 2.
AB A network of interacting proteins controls the activity of cyclin-dependent kinase 2 (Cdk2) (refs 1,2) and governs the entry of higher eukaryotic cells into S phase. Analysis of this and other genetic regulatory networks would be facilitated by intracellular reagents that recognize specific targets and inhibit specific network connections. We report here the expression of a combinatorial library of constrained 20-residue peptides displayed by the active-site loop of Escherichia coli thioredoxin, and the use of a two-hybrid system to select those that bind human Cdk2. These peptide aptamers were designed to mimic the recognition function of the complementarity-determining regions of immunoglobulins. The aptamers recognized different epitopes on the Cdk2 surface with equilibrium dissociation constant in the nanomolar range; those tested inhibited Cdk2 activity. Our results show that peptide aptamers bear some analogies with monoclonal antibodies, with the advantages that they are isolated together with their coding genes, that their small size should allow their structures to be solved, and that they are designated to function inside cells.
ACCESSION NUMBER: 96195065 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8606778
TITLE: Genetic selection of peptide aptamers that recognize and inhibit cyclin-dependent kinase 2.
AUTHOR: Colas P; Cohen B; Jessen T; Grishina I; McCoy J; Brent R
CORPORATE SOURCE: Department of Molecular Biology, Massachusetts General Hospital, Boston, Massachusetts 02114, USA.
SOURCE: Nature, (1996 Apr 11) Vol. 380, No. 6574, pp. 548-50. Journal code: 0410462. ISSN: 0028-0836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199605
ENTRY DATE: Entered STN: 31 May 1996
Last Updated on STN: 6 Feb 1998
Entered Medline: 20 May 1996

L5 ANSWER 5 OF 7 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
TI Production of soluble mammalian proteins in Escherichia coli: identification of protein features that correlate with successful expression.
AB Background: In the search for generic expression strategies for mammalian protein families several bacterial expression vectors were examined for their ability to promote high yields of soluble protein. Proteins studied included cell surface receptors (Ephrins and Eph receptors, CD44), kinases (EGFR-cytoplasmic domain, CDK2 and 4), proteases (MMP1, CASP2), signal transduction proteins (GRB2, RAF1, HRAS) and transcription factors (GATA2, Fli1, Trp53, Mdm2, JUN, FOS, MAD, MAX). Over 400 experiments were performed where expression of 30 full-length proteins and protein domains were evaluated with 6 different N-terminal and 8 C-terminal fusion partners. Expression of an additional set of 95 mammalian proteins was also performed to test the conclusions of this study. Results: Several protein features correlated with soluble protein expression yield including molecular weight and the number of contiguous hydrophobic residues and low complexity regions. There was no relationship between successful expression and protein pI, grand average of hydropathicity (GRAVY), or sub-cellular location. Only small globular cytoplasmic proteins with an average molecular weight of 23 kDa did not require a solubility enhancing tag for high level soluble expression. Thioredoxin (Trx) and maltose binding protein (MBP) were the best

N-terminal protein fusions to promote soluble expression, but MBP was most effective as a C-terminal fusion. 63 of 95 mammalian proteins expressed at soluble levels of greater than 1 mg/l as N-terminal H10-MBP fusions and those that failed possessed, on average, a higher molecular weight and greater number of contiguous hydrophobic amino acids and low complexity regions. Conclusions: By analysis of the protein features identified here, this study will help predict which mammalian proteins and domains can be successfully expressed in E. coli as soluble product and also which are best targeted for a eukaryotic expression system. In some cases proteins may be truncated to minimise molecular weight and the numbers of contiguous hydrophobic amino acids and low complexity regions to aid soluble expression in E. coli.

ACCESSION NUMBER: 2005:159023 BIOSIS
DOCUMENT NUMBER: PREV200500160892
TITLE: Production of soluble mammalian proteins in Escherichia coli: identification of protein features that correlate with successful expression.
AUTHOR(S): Dyson, Michael R. [Reprint Author]; Shadbolt, S. Paul; Vincent, Karen J.; Perera, Rajika L.; McCafferty, John
CORPORATE SOURCE: Atlas Gene Express Project, Wellcome Trust Sanger Inst, Wellcome Trust Genome Campus, Cambridge, CB10 1SA, UK mrd@sanger.ac.uk; ps3@sanger.ac.uk; kjv@sanger.ac.uk; rlp@sanger.ac.uk; jm9@sanger.ac.uk
SOURCE: BMC Biotechnology, (December 14 2004) Vol. 4, No. December 14. print.
E-ISSN: 1472-6750 (ISSN online).
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 27 Apr 2005
Last Updated on STN: 27 Apr 2005

L5 ANSWER 6 OF 7 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
TI Selenium metabolism, selenoproteins and mechanisms of cancer prevention: Complexities with thioredoxin reductase.
AB Numerous studies in animal models and more recent studies in humans have demonstrated cancer chemopreventive effects with Se. There is extensive evidence that monomethylated forms of Se are critical metabolites for chemopreventive effects of Se. Induction of apoptosis in transformed cells is an important chemopreventive mechanism. Apoptosis can be triggered by micromolar levels of monomethylated forms of Se independent of DNA damage and in cells having a null p53 phenotype. Cell cycle protein kinase cdk2 and protein kinase C are strongly inhibited by various forms of Se. Inhibitory mechanisms involving modification of cysteine residues in proteins by Se have been proposed that involve formation of Se adducts of the selenotrisulfide (S-Se-S) or selenenylsulfide (S-Se) type or catalysis of disulfide formation. Selenium may facilitate reactions of protein cysteine residues by the transient formation of more reactive S-Se intermediates. A novel chemopreventive mechanism is proposed involving Se catalysis of reversible cysteine/disulfide transformations that occur in a number of redox-regulated proteins, including transcription factors. A time-limited activation mechanism for such proteins, with deactivation facilitated by Se, would allow normalization of critical cellular processes in the early stages of transformation. There is uncertainty at the present time regarding the role of selenoproteins in chemoprevention model systems where supranutritional levels of Se are employed. Mammalian thioredoxin reductase is one selenoprotein that shows increased activity with Se supplementation in the nutritional to supranutritional range. Enhanced thioredoxin reduction could have beneficial effects in oxidative stress, but possible adverse effects are considered. Other functions of thioredoxin reductase may be relevant to cell signaling pathways. The functional status of the thioredoxin/ thioredoxin reductase system during in vivo chemoprevention with Se has not been established. Some in vitro studies have shown inhibitory

effects of Se on the thioredoxin system correlated with growth inhibition by Se. A potential inactivating mechanism for thioredoxin reductase or other selenoenzymes involving formation of a stable diselenide form resistant to reduction is discussed. New aspects of Se biochemistry and possible functions of new selenoproteins in chemoprevention are described.

ACCESSION NUMBER: 1999:480208 BIOSIS
DOCUMENT NUMBER: PREV199900480208
TITLE: Selenium metabolism, selenoproteins and mechanisms of cancer prevention: Complexities with thioredoxin reductase.
AUTHOR(S): Ganther, Howard E. [Reprint author]
CORPORATE SOURCE: Department of Nutritional Sciences, University of Wisconsin, 1415 Linden Drive, Madison, WI, 53706, USA
SOURCE: Carcinogenesis (Oxford), (Sept., 1999) Vol. 20, No. 9, pp. 1657-1666. print.
CODEN: CRNGDP. ISSN: 0143-3334.
DOCUMENT TYPE: Article
General Review; (Literature Review)
LANGUAGE: English
ENTRY DATE: Entered STN: 9 Nov 1999
Last Updated on STN: 9 Nov 1999

L5 ANSWER 7 OF 7 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
TI Genetic selection of peptide aptamers that recognize and inhibit cyclin-dependent kinase 2.
AB A network of interacting proteins controls the activity of cyclindependent kinase 2 (Cdk2) (refs 1, 2) and governs the entry of higher eukaryotic cells into S phase. Analysis of this and other genetic regulatory networks would be facilitated by intracellular reagents that recognize specific targets and inhibit specific network connections. We report here the expression of a combinatorial library of constrained 20-residue peptides displayed by the active-site loop of Escherichia coli thioredoxin, and the use of a two-hybrid system to select those that bind human Cdk2. These peptide aptamers were designed to mimic the recognition function of the complementarity-determining regions of immunoglobulins. The aptamers recognized different epitopes on the Cdk2 surface with equilibrium dissociation constant in the nanomolar range; those tested inhibited Cdk2 activity. Our results show that peptide aptamers bear some analogies with monoclonal antibodies, with the advantages that they are isolated together with their coding genes, that their small size should allow their structures to be solved, and that they are designated to function inside cells.

ACCESSION NUMBER: 1996:218529 BIOSIS
DOCUMENT NUMBER: PREV199698774658
TITLE: Genetic selection of peptide aptamers that recognize and inhibit cyclin-dependent kinase 2.
AUTHOR(S): Colas, Pierre; Cohen, Barak; Jessen, Timm; Grishina, Irina; McCoy, John; Brent, Roger [Reprint author]
CORPORATE SOURCE: Dep. Mol. Biol., Massachusetts General Hosp., 50 Blossom St., Boston, MA 02114, USA
SOURCE: Nature (London), (1996) Vol. 380, No. 6574, pp. 548-550.
CODEN: NATUAS. ISSN: 0028-0836.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 8 May 1996
Last Updated on STN: 10 Jun 1996

Search Forms
Search Results
Help
User Searches
Preferences
Logout

Refine Search

Search Results -

Terms	Documents
L7 and L6	0

Database:
US Pre-Grant Publication Full-Text Database
US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search: L8

Refine Search

Recall Text Clear Interrupt

Search History

DATE: Saturday, February 10, 2007 **Purge Queries** Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT; PLUR=YES; OP=OR			
L8	L7 and l6	0	L8
L7	colas.in.	116	L7
L6	L5 and (Cdk2)	701	L6
L5	L4 and (pro-apoptotic protein)	26225	L5
L4	L3 and (cyclin-dependent kinase)	26225	L4
L3	L2 and (intracellular recognition molecule)	70171	L3
L2	L1 and (peptide aptamer)	77218	L2
L1	(thioredoxin and TRX-like protein)	177593	L1

END OF SEARCH HISTORY